

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/983,000

DATE: 11/02/2001

TIME: 15:30:46

Input Set : A:\es.txt

Output Set: N:\CRF3\11022001\I983000.raw

**Does Not Comply
Corrected Diskette Needed**

*Errors on pp. 1,3,5, + on sequences as
noted below.*

3 <110> APPLICANT: AGY Therapeutics
4 Melcher, Thorsten
5 Mueller, Sabine
6 Chin, Daniel
8 <120> TITLE OF INVENTION: USE OF PROTEIN BIOMOLECULAR TARGETS IN THE TREATMENT AND
VISUALIZATION OF
9 BRAIN TUMORS
11 <130> FILE REFERENCE: 263/180 -- PEagleman -- AGY
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/983,000
C--> 13 <141> CURRENT FILING DATE: 2001-10-17
13 <160> NUMBER OF SEQ ID NOS: 35
15 <170> SOFTWARE: PatentIn version 3.1

ERRORED SEQUENCES

6210 <210> SEQ ID NO: 23
6211 <211> LENGTH: 3143
6212 <212> TYPE: DNA
6213 <213> ORGANISM: Homo sapiens
6215 <220> FEATURE:
W--> 6216 <221> NAME/KEY: REFERENCE
6217 <222> LOCATION: (1)..(3143)
6218 <223> OTHER INFORMATION: Crosby, A.H., Edwards, S.J., Murray, J.C. and Dixon, M.J.
TITLE G
6219 enomic organization of the human osteopontin gene: exclusion of t
6220 he locus from a causative role in the pathogenesis of dentinogene
6221 sis imperfecta type II JOURNAL Genomics 27 (1), 155-160 (1995)
6224 <220> FEATURE:
6225 <221> NAME/KEY: Gene
6226 <222> LOCATION: (1)..(3143)
6227 <223> OTHER INFORMATION: Osteopontin
6230 <220> FEATURE:
6231 <221> NAME/KEY: CDS
6232 <222> LOCATION: (374)..(427)
6233 <223> OTHER INFORMATION:
6236 <220> FEATURE:
6237 <221> NAME/KEY: CDS
6238 <222> LOCATION: (537)..(575)
6239 <223> OTHER INFORMATION:
6242 <220> FEATURE:
6243 <221> NAME/KEY: CDS
6244 <222> LOCATION: (884)..(964)
6245 <223> OTHER INFORMATION:
6248 <220> FEATURE:
6249 <221> NAME/KEY: CDS
6250 <222> LOCATION: (1232)..(1273)
6251 <223> OTHER INFORMATION:

*The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.*

for Seq. 6, 7, 11, 13, 15, 17, 19, 21

*Please see Sec. 1.823 of the Rules.
This information belongs in the
<3007> to <309> fields*

*Please see example
proper
Attached.*

6254 <220> FEATURE:

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Input Set : A:\es.txt

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6255 <221> NAME/KEY: CDS
 6256 <222> LOCATION: (1597)..(1920)
 6257 <223> OTHER INFORMATION:
 6260 <220> FEATURE:
 6261 <221> NAME/KEY: CDS
 6262 <222> LOCATION: (2305)..(2709)
 6263 <223> OTHER INFORMATION:

discrepancy:
 E--> 6266 <400> SEQUENCE: 33 → *<2107 is listed as 23*

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6267 ggggaagtgt gggagcaggt gggctgggca gtggcagaaa cctgatgaca caatctcgcc      60
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6271 gtcagcagca gcaggaggag gcagagacag catcgtcggg accagactcg tctcaggcca      180
6273 gttgcagcct tctcagccaa acgccgacca aggtacagct tcagtttgct actgggttgt      240
6275 gcattcagct gaatttcatt gggaagtcca aattctaagg aaaaaaatgt ggtagtataa      300
6277 aaaggtatca ctgttgtaac ctatgaagat gtcagctatt cctttgaaat attttgcagg      360
6279 aaaactcact acc atg aga att gca gtg att tgc ttt tgc cta ggc      409
6280                               Met Arg Ile Ala Val Ile Cys Phe Cys Leu Leu Gly
6281                               1                               5                               10
6283 atc acc tgt gcc ata cca gtgagtacag ttgcatctta aagaaaattc      457
6284 Ile Thr Cys Ala Ile Pro
6285                               15
6287 ctgaaaataa ctgaattgtg tgcttccatg tgctaggagg acattcttgt aatctttctt      517
6289 catcttttct gtttctaag gtt aaa cag gct gat tct gga agt tct gag gaa      569
6290                               Val Lys Gln Ala Asp Ser Gly Ser Ser Glu Glu
6291                               20                               25
6293 aag cag gtaagcatct tttatgtttt tatatagtta aatcatttac tcaattatgg      625
6294 Lys Gln
6295 30
6297 cgagaggtgc aagaaacgta tttgctgcga tcaaagtgt tcatatttgt aaagcaattt      685
6299 gaaagagtgc ctagcccaca gtaagtgcta cataagagtt tgtaaataa atctgcaaaa      745
6301 aaaaaaaaaa ttacaaaaag gtacctaagg gtccgggtga ctatatgctt ccatcaagac      805
6303 tagtgaagaa tggttgtttt ttccattcat cctacattt ctttttttaa taatgataaa      865
6305 catgcaactt ttttgtag ctt tac aac aaa tac cca gat gct gtg gcc aca      916
6306                               Leu Tyr Asn Lys Tyr Pro Asp Ala Val Ala Thr
6307                               35                               40
6309 tgg cta aac cct gac cca tct cag aag cag aat ctc cta gcc cca cag      964
6310 Trp Leu Asn Pro Asp Pro Ser Gln Lys Gln Asn Leu Leu Ala Pro Gln
6311                               45                               50                               55
6313 gtatttttaa acttctcata attaaactac agtgatgaaa gatagccaca ctgaggccat      1024
6315 ttgggtgctc cagatgaatc ctgccctgcc tgctggcaaa catgtgctta ggacattgac      1084
6317 tgatctgcca tgttggtctt tctctgtgtt aagccatcca cagatgaggc tgaaaaataa      1144
6319 aaactgcttt ggattaaaaa ggtaaacttt tgaataaaaa agctaggcat gtgtgatgcy      1204
6321 cactaacacg tgccattcct tcttcag aat gct gtg tcc tct gaa gaa acc aat      1258
6322                               Asn Ala Val Ser Ser Glu Glu Thr Asn
6323                               60                               65
6325 gac ttt aaa caa gag gtaagttctc attttcaatc agaggcccat catgccttga      1313
6326 Asp Phe Lys Gln Glu
6327                               70
6329 agagatgaaa gaaggcattg cctggattct cttctgatga aatttcatta gcaagttttc      1373
6331 cagctaattg gcagtctaaa acttgctcat aaataaaaca tgtatttact aaatatcaga      1433

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6333	aataactagggt	ttcctcgggat	aacctaataag	ccatgggtatg	tactgtgaat	gcaaagattc	1493
6335	tgaaactaaa	taaaaagaaa	gatagtaaaa	gactaatgtg	ctataaaggc	taagggaata	1553
6337	taaaaaccca	tatattaatt	ttcccggcca	tcttaatttt	cag acc ctt cca agt		1608
6338					Thr Leu Pro Ser		
6339					75		
6341	aag tcc aac gaa agc cat gac cac atg gat gat atg gat gat gaa gat						1656
6342	Lys Ser Asn Glu Ser His Asp His Met Asp Asp Met Asp Asp Glu Asp						
6343		80		85		90	
6345	gat gat gac cat gtg gac agc cag gac tcc att gac tcg aac gac tct						1704
6346	Asp Asp Asp His Val Asp Ser Gln Asp Ser Ile Asp Ser Asn Asp Ser						
6347		95		100		105	
6349	gat gat gta gat gac act gat gat tct cac cag tct gat gag tct cac						1752
6350	Asp Asp Val Asp Asp Thr Asp Asp Ser His Gln Ser Asp Glu Ser His						
6351		110		115		120	
6353	cat tct gat gaa tct gat gaa ctg gtc act gat ttt ccc acg gac ctg						1800
6354	His Ser Asp Glu Ser Asp Thr Asp Asp Ser His Gln Ser Asp Glu Ser His						
6355	125		130		135		140
6357	cca gca acc gaa gtt ttc act cca gtt gtc ccc aca gta gac aca tat						1848
6358	Pro Ala Thr Glu Val Phe Thr Pro Val Val Pro Thr Val Asp Thr Tyr						
6359		145		150		155	
6361	gat ggc cga ggt gat agt gtg gtt tat gga ctg agg tca aaa tct aag						1896
6362	Asp Gly Arg Gly Asp Ser Val Val Tyr Gly Leu Arg Ser Lys Ser Lys						
6363		160		165		170	
6365	aag ttt cgc aga cct gac atc cag gtaaatcctt taacagacac acctgatggt						1950
6366	Lys Phe Arg Arg Pro Asp Ile Gln						
6367		175		180			
6369	tctgactagc gctcaagtct aggaataccac agtttgcata ttcattcatt cattcatcca						2010
6371	ttcattcatt cattcagcaa gaattcattc atattctact ttatgacat tgaatacaaa						2070
6373	tctttttctg cttggcgggt tttgtaagtc tacataattt ctctctagat ttgattctca						2130
6375	aacacaattc tactttttga aatcctggat caaagtaaca tgctagtatt atttcagcca						2190
6377	gatttagaca atttttagta taagatgacc taaaagctag agagtggaaa aggattacca						2250
6379	tattcccatc cctagccggt catataatta ttcttcattt gtgccgtgat tcag tac						2307
6380						Tyr	
6383	cct gat gct aca gac gag gac atc acc tca cac atg gaa agc gag gag						2355
6384	Pro Asp Ala Thr Asp Glu Asp Ile Thr Ser His Met Glu Ser Glu Glu						
6385		185		190		195	
6387	ttg aat ggt gca tac aag gcc atc ccc gtt gcc cag gac ctg aac gcg						2403
6388	Leu Asn Gly Ala Tyr Lys Ala Ile Pro Val Ala Gln Asp Leu Asn Ala						
6389		200		205		210	
6391	cct tct gat tgg gac agc cgt ggg aag gac agt tat gaa acg agt cag						2451
6392	Pro Ser Asp Trp Asp Ser Arg Gly Lys Asp Ser Tyr Glu Thr Ser Gln						
6393		215		220		225	
6395	ctg gat gac cag agt gct gaa acc cac agc cac aag cag tcc aga tta						2499
6396	Leu Asp Asp Gln Ser Ala Glu Thr His Ser His Lys Gln Ser Arg Leu						
6397	230		235		240		245
6399	tat aag cgg aaa gcc aat gat gag agc aat gag cat tcc gat gtg att						2547
6400	Tyr Lys Arg Lys Ala Asn Asp Glu Ser Asn Glu His Ser Asp Val Ile						
6401		250		255		260	
6403	gat agt cag gaa ctt tcc aaa gtc agc cgt gaa ttc cac agc cat gaa						2595

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6404 Asp Ser Gln Glu Leu Ser Lys Val Ser Arg Glu Phe His Ser His Glu
6405          265          270          275
6407 ttt cac agc cat gaa gat atg ctg gtt gta gac ccc aaa agt aag gaa      2643
6408 Phe His Ser His Glu Asp Met Leu Val Val Asp Pro Lys Ser Lys Glu
6409          280          285          290
6411 gaa gat aaa cac ctg aaa ttt cgt att tct cat gaa tta gat agt gca      2691
6412 Glu Asp Lys His Leu Lys Phe Arg Ile Ser His Glu Leu Asp Ser Ala
6413          295          300          305
6415 tct tct gag gtc aat taa aaggagaaaa aatacaattt ctcaactttgc      2739
6416 Ser Ser Glu Val Asn
6417 310
6419 atttagtcaa aagaaaaaat gctttatagc aaaatgaaag agaacatgaa atgcttcttt      2799
6421 ctcaagtttat tgggtgaatg tgtatctatt tgagtctgga aataactaat gtgtttgata      2859
6423 attagtttag ttgttggtt catggaaact ccctgtaaac aaaagcttca gggttatgtc      2919
6425 tatgttcatt ctatagaaga aatgcaaact atcactgtat tttaatatatt gttattctct      2979
6427 catgaataga aatttatgta gaagcaaaca aaatactttt acccacttaa aaagagaata      3039
6429 taacatttta tgtcactata atcttttggt ttttaagtta gtgtatattt tgttgtgatt      3099
6431 atcttttgtg gtgtgaataa atcttttatc ttgaatgtaa taag      3143
6569 <210> SEQ ID NO: 25
6570 <211> LENGTH: 259
6571 <212> TYPE: PRT
6572 <213> ORGANISM: Homo sapiens
6574 <220> FEATURE:
6575 <221> NAME/KEY: Gene
6576 <222> LOCATION: (1)..(259)
6577 <223> OTHER INFORMATION: Carbonic Anhydrase domain of human carbonic anhydrase III
E-> 6580 <400> SEQUENCE: 41 → discrepancy!
6582 Ala Lys Glu Trp Gly Tyr Ala Ser His Asn Gly Pro Asp His Trp His
6583 1          5          10          15
6586 Glu Leu Phe Pro Asn Ala Lys Gly Glu Asn Gln Ser Pro Ile Glu Leu
6587          20          25          30
6590 His Thr Lys Asp Ile Arg His Asp Pro Ser Leu Gln Pro Trp Ser Val
6591          35          40          45
6594 Ser Tyr Asp Gly Gly Ser Ala Lys Thr Ile Leu Asn Asn Gly Lys Thr
6595          50          55          60
6598 Cys Arg Val Val Phe Asp Asp Thr Tyr Asp Arg Ser Met Leu Arg Gly
6599 65          70          75          80
6602 Gly Pro Leu Pro Gly Pro Tyr Arg Leu Arg Gln Phe His Leu His Trp
6603          85          90          95
6606 Gly Ser Ser Asp Asp His Gly Ser Glu His Thr Val Asp Gly Val Lys
6607          100         105         110
6610 Tyr Ala Ala Glu Leu His Leu Val His Trp Asn Pro Lys Tyr Asn Thr
6611          115         120         125
6614 Phe Lys Glu Ala Leu Lys Gln Arg Asp Gly Ile Ala Val Ile Gly Ile
6615          130         135         140
6618 Phe Leu Lys Ile Gly His Glu Asn Gly Glu Phe Gln Ile Phe Leu Asp
6619 145         150         155         160
6622 Ala Leu Asp Lys Ile Lys Thr Lys Gly Lys Glu Ala Pro Phe Thr Lys
6623          165         170         175

```

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```
6626 Phe Asp Pro Ser Cys Leu Phe Pro Ala Cys Arg Asp Tyr Trp Thr Tyr
6627           180           185           190
6630 Gln Gly Ser Phe Thr Thr Pro Pro Cys Glu Glu Cys Ile Val Trp Leu
6631           195           200           205
6634 Leu Leu Lys Glu Pro Met Thr Val Ser Ser Asp Gln Met Ala Lys Leu
6635           210           215           220
6638 Arg Ser Leu Leu Ser Ser Ala Glu Asn Glu Pro Pro Val Pro Leu Val
6639 225           230           235           240
6642 Ser Asn Trp Arg Pro Pro Gln Pro Ile Asn Asn Arg Val Val Arg Ala
6643           245           250           255
6646 Ser Phe Lys
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/983,000

DATE: 11/02/2001

TIME: 15:30:48

Input Set : A:\es.txt

Output Set: N:\CRF3\11022001\I983000.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1900 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:1915 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:2762 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:2768 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:3408 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:4386 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
L:4392 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:4786 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:5392 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17
L:5644 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19
L:5650 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:6030 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21
L:6036 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:6216 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:23
L:6266 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:23 differs:33
L:6580 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:25 differs:41

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<110> Smith, John; Smithgene Inc.

<120> Example of a Sequence Listing

<130> 01-00001

<140> PCT/EP98/00001
<141> 1998-12-31

<150> US 08/999,999
<151> 1997-10-15

<160> 4

<170> PatentIn version 2.0

<210> 1
<211> 389
<212> DNA
<213> Paramecium sp.

<220>
<221> CDS
<222> (279)...(389)

<300>
<301> Doc, Richard
<302> Isolation and Characterization of a Gene Encoding a
Protease from Paramecium sp.
<303> Journal of Genes
<304> 1
<305> 4
<306> 1-7
<307> 1988-06-31
<308> 123456
<309> 1988-06-31

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tgatgtggca attgctggca gtgccacagg ctttccagcc aggccttaggg tgggttccgc 180
cgcggcgcgg cggccccctt cgcgctctct tcgcgctctt ctctcgtctt cctctcgtct 240

Appendix 3, page 2

ggacctgatt	aggtagagcag	gaggagggggg	cagtttagc	atg Met 1	gtt Val	tca Ser	atg Met	ttc Phe 5	agc Ser	296						
ttg Leu	tct Ser	ttc Phe	aaa Lys 10	tgg Trp	cct Pro	gga Gly	ttt Phe	tgt Cys 15	ttg Leu	ttt Phe	gtt Val	tgt Cys	ttg Leu 20	ttc Phe	caa Gln	344
tgt Cys	ccc Pro	aaa Lys 25	gtc Val	ctc Leu	ccc Pro	tgt Cys	cac His 30	tca Ser	tca Ser	ctg Leu	cag Gln	ccg Pro 35	aat Asn	ctt Leu	389	

<210> 2
<211> 37
<212> PRT
<213> Paramecium sp.

<400> 2	Met	Val	Ser	Met	Phe	Ser	Leu	Ser	Phe	Lys	Trp	Pro	Gly	Phe	Cys	Leu
	1				5					10					15	
	Phe	Val	Cys	Leu	Phe	Gln	Cys	Pro	Lys	Val	Leu	Pro	Cys	His	Ser	Ser
				20					25					30		
	Leu	Gln	Pro	Asn	Leu											
			35													

<210> 3
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed peptide based on size and polarity to act as a linker between the alpha and beta chains of Protein XYZ.

<400> 3	Met	Val	Asn	Leu	Glu	Pro	Met	His	Thr	Glu	Ile
	1				5					10	

<210> 4
<400> 4
000

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[Annex VIII follows]

identifiers and their accompanying information as shown in the following table. The numeric identifier shall be used only in the "Sequence Listing." The order and presentation of the items of information in the "Sequence Listing" shall conform to the arrangement given below. Each item of information shall begin on a new line and shall begin with the numeric identifier enclosed in angle brackets as shown. The submission of those items of information designated with an "M" is mandatory. The submission of those items of information designated with an "O" is optional. Numeric identifiers <110> through <170> shall only be set forth at the beginning of the "Sequence Listing." The following table illustrates the numeric identifiers.

Numeric Identifier	Definition	Comments and Format	Mandatory (M) or Optional (O)
<110>	Applicant	Preferably max. of 10 names; one name per line; preferable format: Surname, Other Names and/or Initials	M
<120>	Title of Invention		M
<130>	File Reference	Personal file reference	M, when filed prior to assignment of appl. number
<140>	Current Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if available
<141>	Current Filing Date	Specify as: yyyy-mm-dd	M, if available
<150>	Prior Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if applicable include priority documents under 35 USC 119 and 120
<151>	Prior Application Filing Date	Specify as: yyyy-mm-dd	M, if applicable
<160>	Number of SEQ ID NOs	Count includes total number of SEQ ID NOs	M
<170>	Software	Name of software used to create the Sequence Listing	O
<210>	SEQ ID NO:#:	Response shall be an integer representing the SEQ ID NO shown	M
<211>	Length	Respond with an integer expressing the number of bases or amino acid residues	M

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<212>	Type	Whether presented sequence molecule is DNA, RNA, or PRT (protein). If a nucleotide sequence contains both DNA and RNA fragments, the type shall be "DNA." In addition, the combined DNA/RNA molecule shall be further described in the <220> to <223> feature section.	M
<213>	Organism	Scientific name, i.e. Genus/species, Unknown or Artificial Sequence. In addition, the "Unknown" or "Artificial Sequence" organisms shall be further described in the <220> to <223> feature section.	M
<220>	Feature	Leave blank after <220>. <221-223> provide for a description of points of biological significance in the sequence.	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<221>	Name/Key	Provide appropriate identifier for feature, preferably from WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence
<222>	Location	Specify location within sequence; where appropriate state number of first and last bases/amino acids	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified

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		in feature	base was used in a sequence
<223>	Other Information	Other relevant information; four lines maximum	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<300>	Publication Information	Leave blank after <300>	0
<301>	Authors	Preferably max of ten named authors of publication; specify one name per line; preferable format: Surname, Other Names and/or Initials	0
<302>	Title		0
<303>	Journal		0
<304>	Volume		0
<305>	Issue		0
<306>	Pages		0
<307>	Date	Journal date on which data published; specify as yyyy-mm-dd, MMM-yyyy or Season-yyyy	0
<308>	Database Accession Number	Accession number assigned by database including database name	0
<309>	Database Entry Date	Date of entry in database; specify as yyyy-mm-dd or MMM-yyyy	0
<310>	Patent Document Number	Document number; for patent-type citations only. Specify as, for example, US 07/999,999	0

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<311>	Patent Filing Date	Document filing date, for patent-type citations only; specify as yyyy-mm-dd	0
<312>	Publication Date	Document publication date, for patent-type citations only; specify as yyyy-mm-dd	0
<313>	Relevant Residues	FROM (position) TO (position)	0
<400>	Sequence	SEQ ID NO should follow the numeric identifier and should appear on the line preceding the actual sequence	0

5. Section 1.024 is revised to read as follows:

1.024 Form and format for nucleotide and/or amino acid sequence submissions in computer readable form.

(a) The computer readable form required by 1.021(c) shall meet the following specifications:

(1) The computer readable form shall contain a single "Sequence Listing" as either a diskette, series of diskettes, or other permissible media outlined in paragraph (c) of this section.

(2) The "Sequence Listing" in paragraph (a) (1) of this section shall be submitted in American Standard Code for Information Interchange (ASCII) text. No other formats shall be allowed.

(3) The computer readable form may be created by any means, such as word processors, nucleotide/amino acid sequence editors or other custom computer programs; however, it shall conform to all specifications detailed in this section.

(4) File compression is acceptable when using diskette media, so long as the compressed file is in a self-extracting format that will decompress on one of the systems described in paragraph (b) of this section.

(5) Page numbering shall not appear within the computer readable form version of the "Sequence Listing" file.

(6) All computer readable forms shall have a label permanently affixed thereto on which has been hand-printed or typed: the name of the applicant, the title of the invention, the date on which the data were recorded on the computer readable form, the operating system used, a reference number, and an application serial number and filing date, if known.

(b) Computer readable form submissions must meet these format requirements:

(1) Computer: IBM PC/XT/AT, or compatibles, or Apple Macintosh;

(2) Operating System: MS-DOS, Unix or Macintosh;

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